

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/575,265
Source: IFWP
Date Processed by STIC: 04/24/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/24/2006

PATENT APPLICATION: US/10/575,265

TIME: 16:16:43

Input Set : A:\08940.0300 Sequence Listing.txt

Output Set: N:\CRF4\04242006\J575265.raw

3 <110> APPLICANT: FIVE PRIME THERAPEUTICS, INC.
 4 WONG, JUSTIN
 5 HESTIR, KEVIN
 6 COLLINS, AMY
 8 <120> TITLE OF INVENTION: KIAA0779, SPLICE VARIANTS THEREOF, AND METHODS OF
 THEIR USE
 10 <130> FILE REFERENCE: 08940.0030-00304
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/575,265
 C--> 13 <141> CURRENT FILING DATE: 2006-04-10
 15 <150> PRIOR APPLICATION NUMBER: 60/510,612
 16 <151> PRIOR FILING DATE: 2003-10-10
 18 <160> NUMBER OF SEQ ID NOS: 38
 20 <170> SOFTWARE: PatentIn version 3.2
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 23 <211> LENGTH: 291
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
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 30 cctcccagat tggatctctt tttcatatgg atcttctgtt tctatgtctt tttaaaaaat 120
 32 aacttttttg gaaacctttt ggattacaac tggtcatcct cacctatgca aagaaagggg 180
 34 agctattgct gggattttga ggagatggtc ctagaacaat tggagattca tacgcacaca 240
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 40 <211> LENGTH: 231
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 49 aacttttttg gaaacctttt ggattacaac tggtcatcct cacctatgca aagaaagggg 180
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 55 <211> LENGTH: 1962
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 57 <213> ORGANISM: Homo sapiens
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 64 gctttggaga acattaacgt gattggccaa ggcttgaagc atctcttcca gcaccagcgc 180
 66 aggaggtcat cagtgtctcc acatgatgtg cagcaaatc aggagatcc agaacctgaa 240
 68 atggatctgg aaagccagaa cgcattgtgct gagattgatg gtgtcccccac ccaccccaca 300
 70 gctctgaatc gtgtcctgca gcagattcga gtgccaccca agatgaagag agggacaagc 360
 72 ttgcatagta ggcggggcaa gccagaggcc ccaaagggaa gtccccaaat caacagggaag 420

cp9-6)

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76 gatgcaccta cgggctctgc tatgatggaa atagcttggt ctgctgctgc tgctgctgct 540
78 gcatgtctac caggagagga gggaactgcg gagcggatcg aacgggttgga agtaagcagc 600
80 cttgccc aaa catccagtgc agtggcctcc agtaccgatg gcagcatcca cacagactct 660
82 gtggatggaa caccagaccc tcagcgcaca aaggctgcca ttgctcacct gcagcagaag 720
84 atcctgaagc tcacagaaca aatcaagatt gcacaaacag cccgggacga caacgttgct 780
86 gaatacttga agcttgccaa cagtgcagac aaacagcagg ctgcccgcag caagcaagtc 840
88 tttgagaaga agaaccagaa atctgccc aa actatcctcc agctgcaaaa gaaacttgag 900
90 cactaccaca ggaagctcag agaggtagag cagaatggga tcccccgga gccaaaggat 960
92 gtcttcaggg acatgcacca ggggtctgaag gatgtaggag caaagggtgac tggcttcagt 1020
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96 gcagcaggcg ctgtagtctc aaagcccaga gagattgcct cactcattcg gaacaaattt 1140
98 ggcagtgcag acaacatccc caacctgaag gactctttag aggaagggca agtggatgat 1200
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106 gcactactac atgagatcca ggagatccgg gaaaccagg ccagactaga ggaatccttt 1440
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112 aatgaaatct tgaacttgaa gcaggaactg gcaagcatgg aagaaaaaat cgcgtatcag 1620
114 tcctatgaac gggcccggga catccaggag gccctggagg catgccagac gcgcatctcc 1680
116 aagatggagc tgcagcagca gcagcagcag gtggtgcagc tagaagggtt ggagaatgcc 1740
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120 ttggtctttg tctccactgt agccaactgt gtggtcccc tcatgaagac tcgcaacagg 1860
122 acgttcagca ctttattcct tgtggttttt attgcctttc tctggaagca ctgggacgcc 1920
124 ctcttcagct atgtggaacg gttcttttca tcccctagat ga 1962
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128 <211> LENGTH: 366
129 <212> TYPE: DNA
130 <213> ORGANISM: Homo sapiens
132 <400> SEQUENCE: 4
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135 gaggcagatg agacgcgcat ctccaagatg gagctgcagc agcagcagca gcagggtggtg 120
137 cagctagaag ggctggagaa tgccactgcc cggaaacctt tgggcaaact catcaacatc 180
139 ctcttggttg tcatggcagt ctttttggtc tttgtctcca ctgtagccaa ctgtgtggtc 240
141 cccctcatga agactcgcaa caggacgttc agcactttat tccttggtgt ttttattgcc 300
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145 agatga
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149 <211> LENGTH: 645
150 <212> TYPE: DNA
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 5
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158 gcttttgaga acattaacgt gattggccaa ggcttgaagc atctcttcca gcaccagcgc 180
160 aggaggtcat cagtgtctcc acatgatgtg cagcaaatc aggagatcc agaactgaa 240
162 atggatctgg aaagccagaa cgcagtgtgt gagattgatg gtgtcccccac ccaccacaca 300
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166 ttgcatagta ggcggggcaa gccagaggcc ccaaagggaa gtccccaat caacaggaag      420
168 tctggtcagg agatgacagc tgttatgcag tcaggccgac ccaggctcttc atccacaact      480
170 gatgcaccta ccagctctgc tatgatggaa atagcttggt ctgctgctgc tgctgctgct      540
172 gcatgtctac caggagaaat gccactgccc ggaaccttct gggcaaactc atcaacatcc      600
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178 <211> LENGTH: 1962
179 <212> TYPE: DNA
180 <213> ORGANISM: Homo sapiens
182 <400> SEQUENCE: 6
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187 gctttggaga acattaacgt gattggccaa ggcttgaagc atctcttcca gcaccagcgc      180
189 aggaggtcat cagtgtctcc acatgatgtg cagcaaattc aggagatcc agaacctgaa      240
191 atggatctgg aaagccagaa cgcagtgtgt gagattgatg gtgtcccccac ccaccccaca      300
193 gctctgaatc gtgtcctgca gcagattcga gtgccaccga agatgaagag agggacaagc      360
195 ttgcatagta ggcggggcaa gccagaggcc ccaaagggaa gtccccaat caacaggaag      420
197 tctggtcagg agatgacagc tgttatgcag tcaggccgac ccaggctcttc atccacaact      480
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207 atcctgaagc tcacagaaca aatcaagatt gcacaaacag cccgggacga caacgttgct      780
209 gaatacttga agcttgccaa cagtgcagac aaacagcagg ctgcccgcac caagcaagtc      840
211 tttgagaaga agaaccagaa atctgcccac actatcctcc agctgcaaaa gaaacttgag      900
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215 gtcttcaggg acatgcacca gggctctgaag gatgtaggag caaagggtgac tggcttcagt      1020
217 gaagggtggg tggatagtgt caaagggtggg ttttccagct tctcccaggc caccatttca      1080
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229 gcactactac atgagatcca ggagatccgg gaaaccagc ccagactaga ggaatccttt      1440
231 gagactctca aggaacatta tcagagggac tattccttaa taatgcagac cttacaggag      1500
233 gagcgatata gatgtgaacg attggaagaa cagctaaatg acctaacaga gctccaccag      1560
235 aatgaaatct tgaacttgaa gcaggaactg gcaagcatgg aagaaaaaat cgcgtatcag      1620
237 tcctatgaac gggcccggga catccaggag gccctggagg catgccagac gcgcatctcc      1680
239 aagatggagc tgcagcagca gcagcagcag gtggtgcagc tagaagggtt ggagaatgcc      1740
241 actgcccgga accttctggg caaactcatc aacatcctcc tggctgtcat ggcagtcctt      1800
243 ttggtctttg tctccactgt agccaactgt gtggtcccc tcatgaagac tcgcaacagg      1860
245 acgttcagca ctttattcct tgtggttttt attgcctttc tctggaagca ctgggacgcc      1920
247 ctcttcagct atgtggaacg gttcttttca tcccctagat ga                      1962
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251 <211> LENGTH: 96
252 <212> TYPE: PRT
253 <213> ORGANISM: Homo sapiens
255 <400> SEQUENCE: 7
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257 1           5           10           15
260 His Ser Val His Pro Pro Arg Leu Asp Leu Phe Phe Ile Trp Ile Phe
261           20           25           30
264 Cys Phe Tyr Val Phe Leu Lys Asn Asn Phe Leu Gly Asn Leu Leu Asp
265           35           40           45
268 Tyr Asn Cys Ser Ser Ser Pro Met Gln Arg Lys Gly Ser Tyr Cys Trp
269           50           55           60
272 Asp Phe Glu Glu Met Val Leu Glu Gln Leu Glu Ile His Thr His Thr
273 65           70           75           80
276 Lys Asn Leu Asn Pro Tyr Leu Thr Pro Asp Thr Lys Ala Thr Phe Lys
277           85           90           95
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281 <211> LENGTH: 76
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283 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 8
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290 His Ser Val His Pro Pro Arg Leu Asp Leu Phe Phe Ile Trp Ile Phe
291           20           25           30
294 Cys Phe Tyr Val Phe Leu Lys Asn Asn Phe Leu Gly Asn Leu Leu Asp
295           35           40           45
298 Tyr Asn Cys Ser Ser Ser Pro Met Gln Arg Lys Gly Ser Tyr Cys Trp
299           50           55           60
302 Asp Phe Glu Glu Ala Val Arg Cys His Trp Ala Val
303 65           70           75
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307 <211> LENGTH: 653
308 <212> TYPE: PRT
309 <213> ORGANISM: Homo sapiens
311 <400> SEQUENCE: 9
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317           20           25           30
320 Lys Leu Ser Lys Met Thr His Asn Ala Leu Glu Asn Ile Asn Val Ile
321           35           40           45
324 Gly Gln Gly Leu Lys His Leu Phe Gln His Gln Arg Arg Arg Ser Ser
325           50           55           60
328 Val Ser Pro His Asp Val Gln Gln Ile Gln Ala Asp Pro Glu Pro Glu
329 65           70           75           80
332 Met Asp Leu Glu Ser Gln Asn Ala Cys Ala Glu Ile Asp Gly Val Pro
333           85           90           95
336 Thr His Pro Thr Ala Leu Asn Arg Val Leu Gln Gln Ile Arg Val Pro
337           100          105          110
340 Pro Lys Met Lys Arg Gly Thr Ser Leu His Ser Arg Arg Gly Lys Pro
341           115          120          125
344 Glu Ala Pro Lys Gly Ser Pro Gln Ile Asn Arg Lys Ser Gly Gln Glu
345           130          135          140

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352 Asp Ala Pro Thr Gly Ser Ala Met Met Glu Ile Ala Cys Ala Ala Ala
353                               165                               170                               175
356 Ala Ala Ala Ala Ala Cys Leu Pro Gly Glu Glu Gly Thr Ala Glu Arg
357                               180                               185                               190
360 Ile Glu Arg Leu Glu Val Ser Ser Leu Ala Gln Thr Ser Ser Ala Val
361                               195                               200                               205
364 Ala Ser Ser Thr Asp Gly Ser Ile His Thr Asp Ser Val Asp Gly Thr
365                               210                               215                               220
368 Pro Asp Pro Gln Arg Thr Lys Ala Ala Ile Ala His Leu Gln Gln Lys
369 225                               230                               235                               240
372 Ile Leu Lys Leu Thr Glu Gln Ile Lys Ile Ala Gln Thr Ala Arg Asp
373                               245                               250                               255
376 Asp Asn Val Ala Glu Tyr Leu Lys Leu Ala Asn Ser Ala Asp Lys Gln
377                               260                               265                               270
380 Gln Ala Ala Arg Ile Lys Gln Val Phe Glu Lys Lys Asn Gln Lys Ser
381                               275                               280                               285
384 Ala Gln Thr Ile Leu Gln Leu Gln Lys Lys Leu Glu His Tyr His Arg
385                               290                               295                               300
388 Lys Leu Arg Glu Val Glu Gln Asn Gly Ile Pro Arg Gln Pro Lys Asp
389 305                               310                               315                               320
392 Val Phe Arg Asp Met His Gln Gly Leu Lys Asp Val Gly Ala Lys Val
393                               325                               330                               335
396 Thr Gly Phe Ser Glu Gly Val Val Asp Ser Val Lys Gly Gly Phe Ser
397                               340                               345                               350
400 Ser Phe Ser Gln Ala Thr His Ser Ala Ala Gly Ala Val Val Ser Lys
401                               355                               360                               365
404 Pro Arg Glu Ile Ala Ser Leu Ile Arg Asn Lys Phe Gly Ser Ala Asp
405                               370                               375                               380
408 Asn Ile Pro Asn Leu Lys Asp Ser Leu Glu Glu Gly Gln Val Asp Asp
409 385                               390                               395                               400
412 Ala Gly Lys Ala Leu Gly Val Ile Ser Asn Phe Gln Ser Ser Pro Lys
413                               405                               410                               415
416 Tyr Gly Ser Glu Glu Asp Cys Ser Ser Ala Thr Ser Gly Ser Val Gly
417                               420                               425                               430
420 Ala Asn Ser Thr Thr Gly Gly Ile Ala Val Gly Ala Ser Ser Ser Lys
421                               435                               440                               445
424 Thr Asn Thr Leu Asp Met Gln Ser Ser Gly Phe Asp Ala Leu Leu His
425                               450                               455                               460
428 Glu Ile Gln Glu Ile Arg Glu Thr Gln Ala Arg Leu Glu Glu Ser Phe
429 465                               470                               475                               480
432 Glu Thr Leu Lys Glu His Tyr Gln Arg Asp Tyr Ser Leu Ile Met Gln
433                               485                               490                               495
436 Thr Leu Gln Glu Glu Arg Tyr Arg Cys Glu Arg Leu Glu Glu Gln Leu
437                               500                               505                               510
440 Asn Asp Leu Thr Glu Leu His Gln Asn Glu Ile Leu Asn Leu Lys Gln
441                               515                               520                               525
444 Glu Leu Ala Ser Met Glu Glu Lys Ile Ala Tyr Gln Ser Tyr Glu Arg

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220>

to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:38; N Pos. 94,201,211,212,213,214

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:60

M:341 Repeated in SeqNo=38